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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/029,413A

DATE: 04/03/2002
TIME: 11:08:45

Input Set : A:\EP.txt
Output Set: N:\CRF3\04032002\J029413A.raw

```
   3 <110> APPLICANT: Malouf, Nadia
   4        Nichols, Timothy C.
   6 <120> TITLE OF INVENTION: Purified and Isolated Platelet Calcium Channel Nucleic Acids
and
   7        Polypeptides and Therapeutic and Screening Methods Using Same
   9 <130> FILE REFERENCE: 421/29
C-->  11 <140> CURRENT APPLICATION NUMBER: US/10/029,413A
C-->  11 <141> CURRENT FILING DATE: 2002-03-21
  11 <160> NUMBER OF SEQ ID NOS: 29
  13 <170> SOFTWARE: PatentIn version 3.1
  15 <210> SEQ ID NO: 1
  16 <211> LENGTH: 5565
  17 <212> TYPE: DNA
  18 <213> ORGANISM: Homo sapiens
  20 <220> FEATURE:
  21 <221> NAME/KEY: CDS
  22 <222> LOCATION: (1)..(5565)
  23 <223> OTHER INFORMATION:
  26 <400> SEQUENCE: 1
  27 atg gag cca tcc tca ccc cag gat gaa ggc ctg agg aag aaa cag ccc        48
  28 Met Glu Pro Ser Ser Pro Gln Asp Glu Gly Leu Arg Lys Lys Gln Pro
  29 1               5                   10                  15
  31 aag aag cca gtt cct gag att ctg cca agg cca ccc cgg gct ttg ttc        96
  32 Lys Lys Pro Val Pro Glu Ile Leu Pro Arg Pro Pro Arg Ala Leu Phe
  33             20                  25                  30
  35 tgc ctg acc ctg gag aac ccc ctg agg aag gcc tgc atc agc att gta       144
  36 Cys Leu Thr Leu Glu Asn Pro Leu Arg Lys Ala Cys Ile Ser Ile Val
  37         35                  40                  45
  39 gaa tgg aag ccc ttc gag acg atc atc ttg ctc acc atc ttt gcc aat       192
  40 Glu Trp Lys Pro Phe Glu Thr Ile Ile Leu Leu Thr Ile Phe Ala Asn
  41     50                  55                  60
  43 tgt gtg gcc ctg gcc gtg tac ctg ccc atg ccg gaa gat gac aac aac       240
  44 Cys Val Ala Leu Ala Val Tyr Leu Pro Met Pro Glu Asp Asp Asn Asn
  45 65                  70                  75                  80
  47 tct ctg aac ctc ggc ctg gag aag ctg gag tat ttc ttc ctc att gtc       288
  48 Ser Leu Asn Leu Gly Leu Glu Lys Leu Glu Tyr Phe Phe Leu Ile Val
  49             85                  90                  95
  51 ttc tcg att gaa gcc gcc atg aag atc att gcc tac ggc ttc tta ttc       336
  52 Phe Ser Ile Glu Ala Ala Met Lys Ile Ile Ala Tyr Gly Phe Leu Phe
  53             100                 105                 110
  55 cac cag gac gct tac ctg cgc agt ggc tgg aat gtg ctg gac ttc acc       384
  56 His Gln Asp Ala Tyr Leu Arg Ser Gly Trp Asn Val Leu Asp Phe Thr
  57         115                 120                 125
  59 att gtc ttc ctg ggg gtc ttc acc gtg att ctg gaa cag gtt aac gtc       432
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60  Ile Val Phe Leu Gly Val Phe Thr Val Ile Leu Glu Gln Val Asn Val
61      130                 135                 140
63  atc caa agc cac aca gcc cca atg agc agc aaa gga gcc ggc ttg gat    480
64  Ile Gln Ser His Thr Ala Pro Met Ser Ser Lys Gly Ala Gly Leu Asp
65  145                 150                 155                 160
67  gtc aag gcc ctc aga gcc ttc cga gtg ctc aga ccc ctc cgg ctg gtg    528
68  Val Lys Ala Leu Arg Ala Phe Arg Val Leu Arg Pro Leu Arg Leu Val
69                  165                 170                 175
71  tcg ggg gtg cct agc ctg cag gtg gtc ctg aac tcc atc ttc aag gcc    576
72  Ser Gly Val Pro Ser Leu Gln Val Val Leu Asn Ser Ile Phe Lys Ala
73                  180                 185                 190
75  atg ctc ccc ctc ttt cac atc gcc ctg ctg gtc ctc ttt atg gtc atc    624
76  Met Leu Pro Leu Phe His Ile Ala Leu Leu Val Leu Phe Met Val Ile
77                  195                 200                 205
79  atc tat gcc atc atc ggg ctg gag ctc ttc aag ggc aag atg cac aag    672
80  Ile Tyr Ala Ile Ile Gly Leu Glu Leu Phe Lys Gly Lys Met His Lys
81      210                 215                 220
83  acc tgc tac ttc att ggt aca gat atc gtg gcc acg gtg gag aat gaa    720
84  Thr Cys Tyr Phe Ile Gly Thr Asp Ile Val Ala Thr Val Glu Asn Glu
85  225                 230                 235                 240
87  gag cca tcg ccc tgc gcc agg acg ggc tca ggg cgc cgg tgc acc atc    768
88  Glu Pro Ser Pro Cys Ala Arg Thr Gly Ser Gly Arg Arg Cys Thr Ile
89                  245                 250                 255
91  aat ggc agt gag tgc cgg ggc ggc tgc cca ggg ccc aac cat ggc atc    816
92  Asn Gly Ser Glu Cys Arg Gly Gly Cys Pro Gly Pro Asn His Gly Ile
93                  260                 265                 270
95  acc cac ttc gac aac ttc ggc ttc tcc atg ctc acc gtg tac cag tgc    864
96  Thr His Phe Asp Asn Phe Gly Phe Ser Met Leu Thr Val Tyr Gln Cys
97                  275                 280                 285
99  att acc atg gag gga tgg act gac gtc ctt tac tgg gtc aat gat gcc    912
100 Ile Thr Met Glu Gly Trp Thr Asp Val Leu Tyr Trp Val Asn Asp Ala
101     290                 295                 300
103 atc ggg aat gag tgg ccc tgg atc tat ttt gtc acc ctc att ttg ctg    960
104 Ile Gly Asn Glu Trp Pro Trp Ile Tyr Phe Val Thr Leu Ile Leu Leu
105 305                 310                 315                 320
107 gga tcc ttc ttc atc ctc aac ctg gtg ctg ggt gtc ctg agt ggg gaa   1008
108 Gly Ser Phe Phe Ile Leu Asn Leu Val Leu Gly Val Leu Ser Gly Glu
109                 325                 330                 335
111 ttc acc aag gag cgg gag aag gcc aag tcc agg gga acc ttc cag aag   1056
112 Phe Thr Lys Glu Arg Glu Lys Ala Lys Ser Arg Gly Thr Phe Gln Lys
113                 340                 345                 350
115 ctc cgg gag aag cag caa cta gat gag gac ctt cgg ggc tac atg agc   1104
116 Leu Arg Glu Lys Gln Gln Leu Asp Glu Asp Leu Arg Gly Tyr Met Ser
117                 355                 360                 365
119 tgg atc acg cag ggc gag gtc atg gat gtt gag gac ttc aga gaa gga   1152
120 Trp Ile Thr Gln Gly Glu Val Met Asp Val Glu Asp Phe Arg Glu Gly
121                 370                 375                 380
123 aaa ctg tct ttg gat gaa ggt ggc tct gac aca gag agc ctg tat gaa   1200
124 Lys Leu Ser Leu Asp Glu Gly Gly Ser Asp Thr Glu Ser Leu Tyr Glu
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125 385                    390                    395                    400
127 att gca ggc ttg aac aaa atc atc cag ttc atc cga cat tgg agg cag   1248
128 Ile Ala Gly Leu Asn Lys Ile Ile Gln Phe Ile Arg His Trp Arg Gln
129                    405                    410                    415
131 tgg aac cgc atc ttt cgc tgg aag tgc cat gac atc gtg aag tcc aag   1296
132 Trp Asn Arg Ile Phe Arg Trp Lys Cys His Asp Ile Val Lys Ser Lys
133                    420                    425                    430
135 gtc ttc tat tgg ctg gtg att ctc atc gtt gcc ctc aac acc ctg tct   1344
136 Val Phe Tyr Trp Leu Val Ile Leu Ile Val Ala Leu Asn Thr Leu Ser
137                    435                    440                    445
139 atc gcc tca gag cac cac aac cag ccg cac tgg ctg acc cgt ttg caa   1392
140 Ile Ala Ser Glu His His Asn Gln Pro His Trp Leu Thr Arg Leu Gln
141         450                    455                    460
143 gac att gcc aac cgg gtg ctg ctg tcc ctc ttc acc act gag atg ctg   1440
144 Asp Ile Ala Asn Arg Val Leu Leu Ser Leu Phe Thr Thr Glu Met Leu
145 465                    470                    475                    480
147 atg aag atg tac ggg ctg ggc ctg cgc cag tac ttc atg tct atc ttc   1488
148 Met Lys Met Tyr Gly Leu Gly Leu Arg Gln Tyr Phe Met Ser Ile Phe
149                    485                    490                    495
151 aac cgc ttc gac tgc ttc gtg gtg tgc agc ggt atc ctg gag atc ctg   1536
152 Asn Arg Phe Asp Cys Phe Val Val Cys Ser Gly Ile Leu Glu Ile Leu
153                    500                    505                    510
155 ctg gtg gag tcg ggc gcc atg aca ccc ctg ggc atc tcc gtg ctc cgc   1584
156 Leu Val Glu Ser Gly Ala Met Thr Pro Leu Gly Ile Ser Val Leu Arg
157         515                    520                    525
159 tgc atc cgc ctc ctg agg atc ttc aag atc acc aaa tat tgg acg tcg   1632
160 Cys Ile Arg Leu Leu Arg Ile Phe Lys Ile Thr Lys Tyr Trp Thr Ser
161         530                    535                    540
163 ctg agc aac ctg gtg gca tcc ctg ctc aac tcc atc cgc tcc atc gcc   1680
164 Leu Ser Asn Leu Val Ala Ser Leu Leu Asn Ser Ile Arg Ser Ile Ala
165 545                    550                    555                    560
167 tcc ctg ctg ctg ctg ctc ttc ctc ttc atc gtc atc ttc cgc ctc ctg   1728
168 Ser Leu Leu Leu Leu Leu Phe Leu Phe Ile Val Ile Phe Arg Leu Leu
169                    565                    570                    575
171 ggc atg cag ctc ttt ggg ggg agg tat gac ttt gaa gac aca gaa gta   1776
172 Gly Met Gln Leu Phe Gly Gly Arg Tyr Asp Phe Glu Asp Thr Glu Val
173                    580                    585                    590
175 cgg cgc agc aac ttt gac aac ttt ccc caa gcc ctc atc agc gtc ttc   1824
176 Arg Arg Ser Asn Phe Asp Asn Phe Pro Gln Ala Leu Ile Ser Val Phe
177         595                    600                    605
179 cag gta ctg aca ggg gaa gac tgg acc tca atg atg tac aat ggg atc   1872
180 Gln Val Leu Thr Gly Glu Asp Trp Thr Ser Met Met Tyr Asn Gly Ile
181         610                    615                    620
183 atg gcc tcg agc ggg ccg tcc tac cct ggc atg ctt gtg tgc att tac   1920
184 Met Ala Ser Ser Gly Pro Ser Tyr Pro Gly Met Leu Val Cys Ile Tyr
185 625                    630                    635                    640
187 ttc atc atc ctt ttc gtc tgt ggc aac tac atc ctg ctc aat gtc ttc   1968
188 Phe Ile Ile Leu Phe Val Cys Gly Asn Tyr Ile Leu Leu Asn Val Phe
189                    645                    650                    655
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191 ctg gcc att gcc gtg gac aac ctg gcc gag gcg gag agc ctg act tct   2016
192 Leu Ala Ile Ala Val Asp Asn Leu Ala Glu Ala Glu Ser Leu Thr Ser
193         660             665             670
195 gcc cag aag gcc aag gct gag gag aaa aaa cgc agg aag atg tcc aag   2064
196 Ala Gln Lys Ala Lys Ala Glu Glu Lys Lys Arg Arg Lys Met Ser Lys
197         675             680             685
199 ggt ctc cca gac aag tca gaa gag gag aag tca acg atg gcc aag aag   2112
200 Gly Leu Pro Asp Lys Ser Glu Glu Glu Lys Ser Thr Met Ala Lys Lys
201         690             695             700
203 ctg gag cag aaa ccc aag ggt gag ggc atc ccc acc act gcc aag ctg   2160
204 Leu Glu Gln Lys Pro Lys Gly Glu Gly Ile Pro Thr Thr Ala Lys Leu
205 705             710             715             720
207 aaa atc gat gag ttt gaa tct aat gtc aat gag gtg aag gat ccc tac   2208
208 Lys Ile Asp Glu Phe Glu Ser Asn Val Asn Glu Val Lys Asp Pro Tyr
209         725             730             735
211 ccc tca gcc gac ttc cca ggg gat gac gag gaa gat gag cct gag atc   2256
212 Pro Ser Ala Asp Phe Pro Gly Asp Asp Glu Glu Asp Glu Pro Glu Ile
213         740             745             750
215 ccg ctg agc ccc cga cca cgt ccc ctg gct gag ctg cag ctg aaa gag   2304
216 Pro Leu Ser Pro Arg Pro Arg Pro Leu Ala Glu Leu Gln Leu Lys Glu
217         755             760             765
219 aag gcc gtg ccc att cca gaa gcc agc tcc ttc ttc atc ttc agc ccc.  2352
220 Lys Ala Val Pro Ile Pro Glu Ala Ser Ser Phe Phe Ile Phe Ser Pro
221         770             775             780
223 acc aat aag atc cgt gtc ctg tgt cac cgc atc gtc aat gcc acc tgg   2400
224 Thr Asn Lys Ile Arg Val Leu Cys His Arg Ile Val Asn Ala Thr Trp
225 785             790             795             800
227 ttc acc aac ttc atc ctg ctc ttc atc ctg ctc agc agc gct gca ctg   2448
228 Phe Thr Asn Phe Ile Leu Leu Phe Ile Leu Leu Ser Ser Ala Ala Leu
229         805             810             815
231 gct gcg gaa gac ccc atc cgg gct gat tcc atg aga aat cag atc ctt   2496
232 Ala Ala Glu Asp Pro Ile Arg Ala Asp Ser Met Arg Asn Gln Ile Leu
233         820             825             830
235 aaa cac ttt gac atc ggg ttc acc tct gtc ttc act gtg gag att gtc   2544
236 Lys His Phe Asp Ile Gly Phe Thr Ser Val Phe Thr Val Glu Ile Val
237         835             840             845
239 ctc aag atg acg acc tac gga gcc ttc ctg cac aag ggt tcc ttc tgc   2592
240 Leu Lys Met Thr Thr Tyr Gly Ala Phe Leu His Lys Gly Ser Phe Cys
241         850             855             860
243 cgc aat tac ttc aac atg ctg gac ctg ctg gtg gtg gcc gtg tcc ctc   2640
244 Arg Asn Tyr Phe Asn Met Leu Asp Leu Leu Val Val Ala Val Ser Leu
245 865             870             875             880
247 atc tcc atg gga ctt gag tcc agt gcc atc tcc gtg gtg aag atc ctg   2688
248 Ile Ser Met Gly Leu Glu Ser Ser Ala Ile Ser Val Val Lys Ile Leu
249         885             890             895
251 agg gtg ctg agg gtg ctc cga cca ctc aga gcc atc aac aga gcc aag   2736
252 Arg Val Leu Arg Val Leu Arg Pro Leu Arg Ala Ile Asn Arg Ala Lys
253         900             905             910
255 ggg ttg aag cac gtg gct agg tgc atg ttc gtg gcc atc agc acc atc   2784
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256 Gly Leu Lys His Val Ala Arg Cys Met Phe Val Ala Ile Ser Thr Ile
257         915             920             925
259 ggg aac atc gtg ctg gtc act acc ctc cta cag ttc atg ttt gcc tgc    2832
260 Gly Asn Ile Val Leu Val Thr Thr Leu Leu Gln Phe Met Phe Ala Cys
261         930             935             940
263 atc ggc gtc cag ctc ttc aag ggg aag ttc ttc agg tgc acc gac ttg    2880
264 Ile Gly Val Gln Leu Phe Lys Gly Lys Phe Phe Arg Cys Thr Asp Leu
265 945             950             955             960
267 tcc aag atg aca gag gag gag tgc agg ggc tac tac tac gtg tac aag    2928
268 Ser Lys Met Thr Glu Glu Glu Cys Arg Gly Tyr Tyr Tyr Val Tyr Lys
269             965             970             975
271 gac ggg gac ccc atg cag ata gag ctg cgt cac cgc gag tgg gta cac    2976
272 Asp Gly Asp Pro Met Gln Ile Glu Leu Arg His Arg Glu Trp Val His
273             980             985             990
275 agc gac ttc cac ttc gac aat gtg  ctc tca gcc atg atg  tcc ctc ttc   3024
276 Ser Asp Phe His Phe Asp Asn Val Leu Ser Ala Met Met  Ser Leu Phe
277             995             1000            1005
279 acg gtc  tcc acc ttc gag gga tgg cct cag ctg ctg  tac aag gcc      3069
280 Thr Val Ser Thr Phe Glu Gly Trp Pro Gln Leu Leu Tyr Lys Ala
281     1010            1015            1020
283 ata gac  tcc aat gcg gag gac gtg ggt ccc atc tac  aac aac cgt      3114
284 Ile Asp Ser Asn Ala Glu Asp Val Gly Pro Ile Tyr Asn Asn Arg
285     1025            1030            1035
287 gtg gag  atg gcc atc ttc ttc atc atc tac atc atc  ctc att gcc      3159
288 Val Glu Met Ala Ile Phe Phe Ile Ile Tyr Ile Ile Leu Ile Ala
289     1040            1045            1050
291 ttc ttc  atg atg aac atc ttt gtg ggc ttc gtc att  gtc acc ttc      3204
292 Phe Phe Met Met Asn Ile Phe Val Gly Phe Val Ile Val Thr Phe
293     1055            1060            1065
295 cag gag  cag gga gag act gag tac aag aac tgt gag  ctg gac aag       3249
296 Gln Glu Gln Gly Glu Thr Glu Tyr Lys Asn Cys Glu Leu Asp Lys
297     1070            1075            1080
299 aac cag  cgc caa tgt gta cag tat gcc ctg aag gcc  cgc cca ctg       3294
300 Asn Gln Arg Gln Cys Val Gln Tyr Ala Leu Lys Ala Arg Pro Leu
301     1085            1090            1095
303 agg tgc  tac att ccc aaa aac cca tac cag tac cag  gtg tgg tac       3339
304 Arg Cys Tyr Ile Pro Lys Asn Pro Tyr Gln Tyr Gln Val Trp Tyr
305     1100            1105            1110
307 att gtc  acc tcc tcc tac ttt gaa tac ctg atg ttt  gcc ctc atc      3384
308 Ile Val Thr Ser Ser Tyr Phe Glu Tyr Leu Met Phe Ala Leu Ile
309     1115            1120            1125
311 atg ctc  aac acc atc tgc ctc ggc atg cag cac tac  aac cag tcg       3429
312 Met Leu Asn Thr Ile Cys Leu Gly Met Gln His Tyr Asn Gln Ser
313     1130            1135            1140
315 gag cag  atg aac cac atc tca gac atc ctc aat gtg  gcc ttc act      3474
316 Glu Gln Met Asn His Ile Ser Asp Ile Leu Asn Val Ala Phe Thr
317     1145            1150            1155
319 atc atc  ttc acc ctg gag atg atc ctc aag ctc atg  gcc ttc aag      3519
320 Ile Ile Phe Thr Leu Glu Met Ile Leu Lys Leu Met Ala Phe Lys
```

Use of n and / or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
to ensure a corresponding explanation is present
in the <220> to <223> fields of each sequence
using n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/029,413A**

Input Set : **A:\EP.txt**
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L:11   M:270 C: Current Application Number differs, Replaced Current Application No
L:11   M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:2149 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:2182 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:2208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:2212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:2221 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:2252 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:2283 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:2395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:2396 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:2443 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:2444 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:2447 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:2448 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:2451 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
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L:2683 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:2684 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:4167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:4215 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:4219 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:4223 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:4227 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:4231 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:4235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
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VERIFICATION SUMMARY   DATE: 04/03/2002
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L:4431  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:4435  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:4439  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:4443  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:4447  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:4451  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:11633 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:23
L:11669 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
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